IN THE CLAIMS:

Please amend claims 1 and 2, as set forth in the complete claim listing below. This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A method for handling a <u>bioinformatics</u> database ~~for bioinformatics, in which~~ <u>hosted on</u> a server <u>and storing a plurality of gene sequences,</u> ~~which is associated with a database for storing sequence information related with bioinformatics and connected to each user terminal~~ <u>said server being connected to a plurality of user terminals</u> through a ~~specific~~ communication network, ~~compares a sequence requested from each user terminal with sequences of the database to analyze a result of the comparison, the method comprises;~~ <u>comprising the steps of:</u>

~~(a) a first step of~~ receiving <u>a new user request for comparison of a gene</u> ~~the~~ sequence from ~~the~~ <u>one of said plurality of</u> user terminal<u>s</u> ~~to store it~~ <u>and storing said new user request</u> in a queue;

~~(b) a second step of~~ checking whether ~~or not~~ there ~~exist other~~ <u>are previous requests for</u> <u>comparison of gene</u> sequences ~~to be compared and analyzed~~ <u>earlier stored in said queue</u>~~, simultaneously with the first step~~;

~~(c) a third step of~~ <u>when said checking step determines that there are previous requests for comparison of gene sequences earlier stored in said queue, comparing one of the plurality of gene sequences stored in the bioinformatics database with all of the requests stored in said queue inclusive of said new request and said earlier requests</u> ~~reading the sequence of the current order~~

~~from the database to compare it with all of the sequences stored in the queue when there exist~~

~~other sequences to be compared and analyzed at the second step~~;

identifying any of the requests stored in said queue inclusive of said new request and said

earlier requests that have been fully compared with all sequences stored in the bioinformatics

database;

~~(d) a fourth step of judging whether or not there exists a sequence that has been compared~~

~~and analyzed for all of sequences of the database among the sequences compared and analyzed at~~

~~the third step, and~~ removing any of the identified fully compared requests ~~the corresponding~~

~~sequence~~ from the queue; ~~and,~~

returning to said step of checking whether there are previous sequences stored in the

queue and iteratively performing said checking, comparing, identifying and removing steps until

all user requests have been fully compared with all sequences stored in the bioinformatics

database and all user requests for comparison have been removed from said queue;

wherein said method reduces time necessary for comparing a plurality of user requests

for comparison of gene sequences to the plurality of gene sequences stored in the bioinformatics

database.

~~(e) a fifth step of incrementing the current order by one, initializing the current order~~

~~when all of the sequences of the database have been read and returning to the second step.~~

2. (Currently Amended) A method for handling a bioinformatics database ~~recording~~

~~medium readable by a computer, in which a computer program for executing the first to fifth~~

~~steps~~ according to claim 1, wherein said method is recorded in a recording medium readable by a

computer ~~is recorded~~.